

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:08:00 ; Search time 28.8 Seconds  
(without alignments)  
2701.975 Million cell updates/sec

Title: US-09-911-513-2  
Perfect score: 2738  
Sequence: 1 MKRDHHHHQDKTMMNNE.....MLGWHTRPLIATSAWKLSTN 532

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues 473505  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_17.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	2758	100.0	532	10	O23724 arabidopsis
2	2754	99.9	532	10	O23643 arabidopsis
3	2747.5	99.6	533	10	O23643 arabidopsis
4	2189.5	79.4	587	10	O23642 arabidopsis
5	2185.5	79.2	587	10	O23642 arabidopsis
6	2179.5	79.0	587	10	O23725 arabidopsis
7	1602.5	58.1	630	10	O23725 arabidopsis
8	1595	57.8	625	10	O23725 arabidopsis
9	1594	57.8	623	10	O23725 arabidopsis
10	1587	57.5	511	10	O23725 arabidopsis
11	1581	57.3	662	10	O23725 arabidopsis
12	1552.5	56.3	547	10	O23725 arabidopsis
13	1490	54.0	523	10	O23725 arabidopsis
14	967.5	35.1	493	10	O23725 arabidopsis
15	608.5	22.1	819	10	O23725 arabidopsis
16	602.5	21.8	653	10	O23725 arabidopsis
17	598.5	21.7	653	10	O23725 arabidopsis
18	590.5	21.4	490	10	O23725 arabidopsis
19	590.5	21.4	668	10	O23725 arabidopsis

20	588.5	21.3	658	10	O9CAN3	Q9can3 arabidopsis
21	565.5	20.5	482	10	O9LPR8	Q9lpr8 arabidopsis
22	564	20.4	413	10	O9S7H5	Q9s7h5 arabidopsis
23	562.5	20.4	526	10	O9LPT0	Q9lpt0 arabidopsis
24	561.5	20.4	428	10	O9ZSP2	Q9zsp2 lycopersico
25	531.5	19.3	313	10	O9ZTB1	Q9ztb1 zea mays (m
26	521.5	18.9	617	10	O9LWU9	Q9lwu9 oryza sativ
27	511.5	18.5	405	10	O9FHZ1	Q9fhz1 arabidopsis
28	509.5	18.4	445	10	O9ZWC5	Q9zwc5 arabidopsis
29	506.5	18.4	306	10	O9XE53	Q9xe53 arabidopsis
30	503.5	18.3	447	10	O9ARF6	Q9arf6 capsella ru
31	487.5	17.7	593	10	O9SDQ3	Q9sdq3 arabidopsis
32	481.5	17.5	1502	10	O9LNX6	Q9lnx6 arabidopsis
33	477.5	17.3	610	10	O9LTI5	Q9lti5 arabidopsis
34	473	17.2	584	10	O9FLO3	Q9flo3 arabidopsis
35	453.5	16.4	808	10	O9XE58	Q9xe58 arabidopsis
36	451.5	16.4	352	10	O9XE51	Q9xe51 arabidopsis
37	440	16.0	1336	10	O81074	O81074 arabidopsis
38	431	15.6	284	10	O9XE57	Q9xe57 arabidopsis
39	429	15.6	375	10	O23566	O23566 arabidopsis
40	428	15.5	583	10	O9SNB8	Q9snb8 arabidopsis
41	422.5	15.3	542	10	O9SCR0	Q9scr0 arabidopsis
42	418.5	15.2	287	10	O9MOM5	Q9mom5 arabidopsis
43	412	14.9	325	10	O9XE52	Q9xe52 arabidopsis
44	407	14.8	718	10	O80933	O80933 arabidopsis
45	393.5	14.3	531	10	O9SZF7	Q9szf7 arabidopsis

ALIGNMENTS

RESULT 1

O23724 PRELIMINARY; PRT; 532 AA.

AC O23724; (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE GAI PROTEIN.

GN GAI.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LANDSBERG RECTA;

RX MEDLINE=98051192; PubMed=9389651;

RA Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,

RA Murphy G.P., Harberd N.P.;

RT "The Arabidopsis GAI gene defines a signaling pathway that negatively

RL Genes Dev. 11:3194-3205(1997).

DR EMBL; Y15193; CAA75492.1; -

DR Mendel; 24070; Arabidopsis; 4AF4BC6EC4265503 CRC64;

SQ SEQUENCE 532 AA; 58789 MW; 4AF4BC6EC4265503 CRC64;

Query Match 100.0%; Score 2758; DB 10; Length 532;

Best Local Similarity 100.0%; Pred. No. 8e-204;

Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRDHHHHQDKTMMNNEEDGNGMDLAVLGKVRSSSEMADVAKLEQLEVMMSNVQ 60

Db 1 MKRDHHHHQDKTMMNNEEDGNGMDLAVLGKVRSSSEMADVAKLEQLEVMMSNVQ 60

QY 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPFSSNAEYDLKAIIPGDAILNQFAIDSASS 120

Db 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPFSSNAEYDLKAIIPGDAILNQFAIDSASS 120

QY 121 SNOGGGGDITTTNKRKCSNGVYVETTTATAESTRHVVLVDVDSQNGVRLVHALLACAEVQ 180

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Db 121 SNOGGGGDTYTNKRLKCSNGVVTETTTATAESTRHVLVDSQENGVRVLHALLACAEAVQ 180
Qy 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQPIDHSLSDTLQM 240
Db 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQPIDHSLSDTLQM 240
Qy 241 HYEYTCPYLKFAHFTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAQALALRPGGPPVF 300
Db 241 HYEYTCPYLKFAHFTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAQALALRPGGPPVF 300
Qy 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLASMLELRPSEIE 360
Db 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLASMLELRPSEIE 360
Qy 361 SVAVNSVFELHKLGRPGAIKVLGVVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 420
Db 361 SVAVNSVFELHKLGRPGAIKVLGVVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 420
Qy 421 STLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Db 421 STLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Qy 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
Db 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
RESULT 2
O23643 PRELIMINARY; PRT; 532 AA.
ID O23643
AC O23643;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE REGA2 PROTEIN.
GN REGA2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97379310; PubMed=9237632;
RA "Truong H.N., Caboche M., Daniel-Vedele F.;
RT "Sequence and characterization of two Arabidopsis thaliana cDNAs
RT isolated by functional complementation of a yeast gln3 gdh1 mutant.";
RL FEBS Lett. 410:213-218(1997).
DR EMBL; Y11337; CAA72178.1;
DR Mendel; 24146; Arath; 3051; 24146.
SQ SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;

Query Match 99.9%; Score 2754; DB 10; Length 532;
Best Local Similarity 99.8%; Pred. No. 1.6e-203;
Matches 531; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNVQ 60
Db 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNVQ 60
Qy 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASS 120
Db 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASS 120
Qy 121 SNOGGGGDTYTNKRLKCSNGVVTETTTATAESTRHVLVDSQENGVRVLHALLACAEAVQ 180
Db 121 SNOGGGGDTYTNKRLKCSNGVVTETTTATAESTRHVLVDSQENGVRVLHALLACAEAVQ 180
Qy 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQPIDHSLSDTLQM 240
Db 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRLSPSQPIDHSLSDTLQM 240
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Qy 241 HYEYTCPYLKFAHFTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAQALALRPGGPPVF 300
Db 241 HYEYTCPYLKFAHFTANQAILAEAFQGGKRVHVVDIFSMSGQLQWPAQALALRPGGPPVF 300
Qy 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLASMLELRPSEIE 360
Db 301 RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLASMLELRPSEIE 360
Qy 361 SVAVNSVFELHKLGRPGAIKVLGVVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 420
Db 361 SVAVNSVFELHKLGRPGAIKVLGVVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 420
Qy 421 STLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Db 421 STLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Qy 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
Db 481 HIGSNAFQAASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
RESULT 3
O9LQT8 PRELIMINARY; PRT; 533 AA.
ID O9LQT8
AC O9LQT8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE F10B6.34.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
RA Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
RA Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
RA Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
RT I.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavert A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006917; AAF79228.1; -.
SQ SEQUENCE 533 AA; 58926 MW; 6464B8C129D79528 CRC64;

Query Match 99.6%; Score 2747.5; DB 10; Length 533;
Best Local Similarity 99.8%; Pred. No. 5.1e-203;
Matches 532; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNV 59
Db 1 MKRDHHHHQDKKTTMMNEEDDGNMDELLAVLGKYKRSSEMADVAQKLEQLEVMMSNV 60
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QY 60 QEDDLSQATETVHYNPABLYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSAS 119
|||||
Db 61 QEDDLSQATETVHYNPABLYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSAS 120
|||||
QY 120 SSNOGGGGDTYTNKRLKCSNGVETTTATATSTRHVVLVDSENGVRLVHALLACAEAV 179
|||||
Db 121 SSNOGGGGDTYTNKRLKCSNGVETTTATATSTRHVVLVDSENGVRLVHALLACAEAV 180
|||||
QY 180 QKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ 239
|||||
Db 181 QKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ 240
|||||
QY 240 MHFETCPLKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 299
|||||
Db 241 MHFETCPLKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 300
|||||
QY 300 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 359
|||||
Db 301 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 360
|||||
QY 360 ESVAVNSVFELHKLGRPGAIKDKVLGVVNVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 419
|||||
Db 361 ESVAVNSVFELHKLGRPGAIKDKVLGVVNVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 420
|||||
QY 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
|||||
Db 421 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
|||||
QY 480 AHIGSNAPKQASMLLALFNGGEGYRVESDGCMLGWHTRPLIATSAWKLSN 532
|||||
Db 481 AHIGSNAPKQASMLLALFNGGEGYRVESDGCMLGWHTRPLIATSAWKLSN 533
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RESULT 4
O23642 PRELIMINARY; PRT; 587 AA.
AC O23642
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE RGAL PROTEIN.
GN RGAL
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97379310; PubMed=9237632;
RA Truong H.N., Caboche M., Daniel-Vedele F.;
RT "Sequence and characterization of two Arabidopsis thaliana cDNAs
RT isolated by functional complementation of a yeast gln3 gdh1 mutant.";
RL FEBS Lett. 410:213-218(1997).
DR EMBL; Y11336; CAA72177.1; -
DR Mendel; 24145; Arath;3051;24145.
SQ SEQUENCE 587 AA; 64023 MW; D0A7A3C741FB51EF CRC64;
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Query Match 79.4%; Score 2189.5; DB 10; Length 587;
Best Local Similarity 74.5%; Pred. No. 5e-160;
Matches 441; Conservative 39; Mismatches 43; Indels 69; Gaps 9;

QY 1 MKRDHHH-----HH-----ODKKTMMNDEEDGNGM-DELLAVLGKVRSSSEMA 43
|||||
Db 1 MKRDHHQFQGRLSNHGTSSSSSSSISKDKMMVKKEEDGGNMDDELLAVLGKVRSSSEMA 60
|||||
QY 44 DVAQKLEQLEVMNSVQEDDLSQATETVHYNPABLYTWLDSMLTDLNPP-----SSN--- 96
|||||
Db 61 EVALKLEQLEVMNSVQEDGLSHLATDTVHYNPSELYSMLDNMLSELNPPPLPASSNGLD 120
|||||
QY 97 -----AEDYDLKAIPGDAILNQFAIDSASSNQGGGGDTYTNKRLK-CSN-- 140
|||||
```

```
Db 121 PVLSPETICGFPASDYDLKVIPGNALYQFPADSSSSN-----NONKRLKSCSSPD 172
|||||
QY 141 -----GW-----ETTATATSTRHVVLVDSENGVRLVHALLACAEAV 179
|||||
Db 173 SMVTSSTGTGTOIGVGITVTVTATTAESTRSVILVDSENGVRLVHALLACAEAI 232
|||||
QY 180 QKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ 239
|||||
Db 233 QONNLTLAEALVKQIGCLAVSQAGAMRKVATYFAEALARRIYRLSPQCNQIDHCLSDTLQ 292
|||||
QY 240 MHFETCPLKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 299
|||||
Db 293 MHFETCPLKFAHTANQAILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPP 352
|||||
QY 300 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 359
|||||
Db 353 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEAIHVEFEYRGFVANSIADLDASMLELRPSEI 412
|||||
QY 360 ESVAVNSVFELHKLGRPGAIKDKVLGVVNVQIKPEIFTVVVEQESNHNPSIFLDRFTESLHY 419
|||||
Db 413 EAVAVNSVFELHKLGRPGIEKVLGVVVKQIKPVFTVVVEQESNHNPGPVFLDRFTESLHY 472
|||||
QY 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
|||||
Db 473 YSTLFDLSLEGVPSQDKVMSEVYLGKQICNLVACDGPDRVERHETLSQWRNRFSGGLAP 532
|||||
QY 480 AHIGSNAPKQASMLLALFNGGEGYRVESDGCMLGWHTRPLIATSAWKLSN 531
|||||
Db 533 AHIGSNAPKQASMLLALFNGGEGYRVESDGCMLGWHTRPLIATSAWKLSN 584
|||||
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RESULT 5
O9SLH3 PRELIMINARY; PRT; 587 AA.
AC O9SLH3
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PUTATIVE RGAL, GIBBERELLIN RESPONSE MODULATION PROTEIN.
GN AT2G01570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV: COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
DR EMBL; AC005560; AAC67333.1; -.
SQ SEQUENCE 587 AA; 64035 MW; FC92E7F9408072AA CRC64;
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Query Match 79.2%; Score 2185.5; DB 10; Length 587;
Best Local Similarity 74.3%; Pred. No. 1e-159;
Matches 440; Conservative 39; Mismatches 44; Indels 69; Gaps 9;

QY 1 MKRDHHH-----HH-----ODKKTMMNDEEDGNGM-DELLAVLGKVRSSSEMA 43
|||||
Db 1 MKRDHHQFQGRLSNHGTSSSSSSSISKDKMMVKKEEDGGNMDDELLAVLGKVRSSSEMA 60
|||||
QY 44 DVAQKLEQLEVMNSVQEDDLSQATETVHYNPABLYTWLDSMLTDLNPP-----SSN--- 96
|||||
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Db 61 EVALKLEQLETMNSVQEDGLSHLATDVTVHYNPSELYSWLDMNLSLNPPLPASSNGLD 120  
QY 97 -----AYDLKAIPGDAILNQFAIDSASSSSNOGGGGDTYTNKRLK-CSN-- 140  
Db 121 PVLPSPEICGFPASDYDLKVPIGNAIYQFPALDSSSSN-----NONKRLKSCSPD 172  
QY 141 -----GVV-----ETTATATAESTRHHVVLVDSQENGVRVHALLACAEAV 179  
Db 173 SWMTSTGTGTOIGGVIGTIVTTTTTTTAAAGESTRSVILVDSQENGVRVHALLACAEAI 232  
QY 180 OKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSPIDHSLSDTLQ 239  
Db 233 QONNLTAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSPQNDHCLSDTLQ 292  
QY 240 MHFETCPYLKFAHTANQALILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 299  
Db 293 MHFETCPYLKFAHTANQALILEAFEGKRVHVIDFSMSQGLQWLPALMQALALRPGGPT 352  
QY 300 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 359  
Db 353 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 412  
QY 360 EAVAVNSVFELHKLGRPGAIKVLGVVYNQIKPEITVVVEQESNHNPIFLDRFTESLHY 419  
Db 413 EAVAVNSVFELHKLGRPGGIEKVLGVVYKQIKPVITVVVEQESNHNPIFLDRFTESLHY 472  
QY 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479  
Db 473 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGGLAP 532  
QY 480 AHIGSNAPKQASMLLALFNGGEGYRVEESDGCLMLGWHTRPLIATSANKLST 531  
Db 533 AHLGSNAFKQASMLLSVFNSSQGYRVEESNGCLMLGWHTRPLIATSANKLST 584

RESULT 6  
Q23725 PRELIMINARY; PRT; 587 AA.  
AC O23725; 587 AA.  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE GRS PROTEIN.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,  
RA Murphy G.P., Harberd N.P.;  
RL Genes Dev. 0:0-0(0).  
DR EMBL; Y15194; CAA75493.1; -.  
DR Mendel; 24071; Arath;3051.24071.  
SQ SEQUENCE 587 AA; 64006 MW; F6F6C7738EE7DCA9 CRC64;

Query Match 79.0%; Score 2179.5; DB 10; Length 587;  
Best Local Similarity 74.0%; Pred. No. 3e-159;  
Matches 438; Conservative 41; Mismatches 44; Indels 69; Gaps 9;  
QY 1 MKRDHHH-----HH-----QDKKTMNNEEDGNGM-DELLAVLGKYKRSSEMA 43  
Db 1 MKRDHHQFQGRLSNHTSSSSSISKDKMMVMVKKEDGGNGMDELLAVLGKYKRSSEMA 60  
QY 44 DVAOKLEQLEVMNSVQEDGLSHLATDVTVHYNPSELYSWLDMNLSLNPPLPASSNGLD 96  
Db 61 EVALKLEQLETMNSVQEDGLSHLATDVTVHYNPSELYSWLDMNLSLNPPLPASSNGLD 120  
QY 97 -----AYDLKAIPGDAILNQFAIDSASSSSNOGGGGDTYTNKRLK-CSN-- 140  
Db 97 -----AYDLKAIPGDAILNQFAIDSASSSSNOGGGGDTYTNKRLK-CSN-- 140

Db 121 PVLPSPEICGFPASDYDLKVPIGNAIYQFPALDSSSSN-----NONKRLKSCSPD 172  
QY 141 -----GVV-----ETTATATAESTRHHVVLVDSQENGVRVHALLACAEAV 179  
Db 173 SWMTSTGTGTOIGGVIGTIVTTTTTTTAAAGESTRSVILVDSQENGVRVHALLACAEAI 232  
QY 180 OKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSPIDHSLSDTLQ 239  
Db 233 QONNLTAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSPQNDHCLSDTLQ 292  
QY 240 MHFETCPYLKFAHTANQALILEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPPV 299  
Db 293 MHFETCPYLKFAHTANQALILEAFEGKRVHVIDFSMSQGLQWLPALMQALALRPGGPT 352  
QY 300 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 359  
Db 353 FRLTGIGPPAPDNFDYLVHVGCKLAHLAEATHVEFEYRGFVANSIADLADSMLELRPSDT 412  
QY 360 EAVAVNSVFELHKLGRPGAIKVLGVVYNQIKPEITVVVEQESNHNPIFLDRFTESLHY 419  
Db 413 EAVAVNSVFELHKLGRPGGIEKVLGVVYKQIKPVITVVVEQESNHNPIFLDRFTESLHY 472  
QY 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479  
Db 473 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGGLAP 532  
QY 480 AHIGSNAPKQASMLLALFNGGEGYRVEESDGCLMLGWHTRPLIATSANKLST 531  
Db 533 AHLGSNAFKQASMLLSVFNSSQGYRVEESNGCLMLGWHTRPLIATSANKLST 584

RESULT 7  
Q9ST48 PRELIMINARY; PRT; 630 AA.  
AC Q9ST48; 630 AA.  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).  
GN D8.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoidae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99347734; PubMed=10421366;  
RA Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,  
RA Flintham J.E., Beales J., Fish L.J., Worland A.J., Pellica F.,  
RA Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;  
RT "Green revolution" genes encode mutant gibberellin response  
RT modulators.";  
RL Nature 400:256-261(1999).  
DR EMBL; AJ242530; CAB51557.1; -.  
DR NON\_TER 630 630  
SQ SEQUENCE 630 AA; 66028 MW; 3D56851726C51042 CRC64;

Query Match 58.1%; Score 1602.5; DB 10; Length 630;  
Best Local Similarity 54.0%; Pred. No. 8.1e-115;  
Matches 344; Conservative 68; Mismatches 106; Indels 119; Gaps 15;  
QY 1 MKRDHHHHQD-----KKTMM-----NEEDGNGMDELLAVLGKYKRSSEM 42  
Db 1 MKRE----YDAGGGGDMGSSKDKMMAAAGAGEQEED--VDELLAALGYKVRSSDM 53  
QY 43 ADVAOKLEQLEVM-----SNVQEDD--LSQATETVHYNPSELYSWLDMNLSLNPPLPASSNGLD 93  
Db 54 ADVAOKLEQLEVMNSVQEDGLSHLATDVTVHYNPSELYSWLDMNLSLNPPLPASSNGLD 113  
QY 94 -----SSNAEYDLKAIPGDAILNQFAI 115  
Db 94 -----SSNAEYDLKAIPGDAILNQFAI 115

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Db 114 PAPLPATPAPRLASTSTVTSGAAGAGYFDLPPAVDSSSSSTYALKP-----SPVAA 168
QY 116 DSASSNOG-----GGGDTYTTNKLKCSNG-----VVE-----TTTATAESTR-- 154
Db 169 PSADSTDSAREPKRMRTGGSTSSSSSSSMOGRTRSSVVEAAPATQASAAANGPA 228
QY 155 -HVVLVDQOENGRVLVHALLACAEAVQENLTVAEALVKQIGFLAVSQIGAMRKVATYFA 213
Db 229 VPVVVVDTQEAGIRLVHALLACAEAVQENFSAAEALVKQIPMLASSOGGAMRKVAAVFG 288
QY 214 EALARRIYEL--SPSQSPIDSLDLOMHFYETCPYLKFAHFTANQAILAEAFQCKRRVH 271
Db 289 EALARRVYRFRPPDSSLLDAFADLLHAHFYESCPIYKFAHFTANQAILAEAFACRRVH 348
QY 272 VIDFSNOSGLOWPALMQALALRPGPPVFRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIH 331
Db 349 VVDFGKOGMWPALLQALALRPGPPSERLTGVPQPDDETALQOQGWKLAQFAHTR 408
QY 332 VEFYRGFVANTLADLASMELR-----PSEIESVAVNSVFLKHLKLRGPAIDKVLGVV 387
Db 409 VDFQYRGLVAATLADLEPFMLQPEGDDTDDEPEVIANSVFLKHLRLLAQPGALEKVLGTV 468
QY 388 NQIKPEIETVVOESNHNHSPFLDRFTESLHYSTLFDLSLEGVPSGQ----- 434
Db 469 RAVRPRIVTVVOEAEHNSGTFLDRTESLHYSTLFDLSLEGAGAGSGQSTDASPAAGG 528
QY 435 -DKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNAPKQASML 493
Db 529 TDQVNSEVYLGKQICNVVACGAEATERHETLQWRSLGSGGFAPVHLGSNAYKQASTL 588
QY 494 LALFNGGEGYRVESDGCMLGWHTRPLIATSAMKLS 530
Db 589 LALFAGGEGYRVEEKDGCCLTLGWHTRPLIATSARVA 625

RESULT 8
Q9MB96 PRELIMINARY; PRT; 625 AA.
ID Q9MB96;
AC Q9MB96;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
OS OSGAI.
GN OSGAI.
OC Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. NIPPONBARE;
RC MEDLINE=20179680; PubMed=10713441;
RA Ogawa M., Kusano T., Katsumi M., Sano H.;
RT "Rice gibberellin-insensitive gene homolog, OSGAI, encodes a nuclear-
RT localized protein capable of gene activation at transcriptional
RT level."
RL Gene 245:21-29(2000).
DR EMBL; AB030956; BAA90749.1; -.
SQ SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;
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Query Match 57.8%; Score 1595; DB 10; Length 625;
Best Local Similarity 56.08; Pred. No. 3e-114;
Matches 332; Conservative 67; Mismatches 110; Indels 84; Gaps 10;

QY 19 BEDDNGMDLAVLGYKVRSEMDVAVKLEQLEVM-----SNVQEDLSQATE 70
Db 34 EED---VDELLAALGYKVRSSMDVAVKLEQLEMDMGVSAPGAADDGFGVSHLATD 90
QY 71 TVHYNPAELYTWLDSMLTDLNPP----- 94
Db 91 TVHYNPDLSSWVESLSELNAPLPIPPAPPAARHASTSTVTGGGGGFELPAAADS 150
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QY 95 SNAEYDLK--ALPGDAILNOFAIDSASSN--OGGGDTYTTNKLKCSNG-----VVE 144
Db 151 SSSYIALRPIPLPVVATADPSAASARDTKRMRTGGSTSSSSSSSLGGGAARGSVVE 210
QY 145 TTTATAESTR-----HVVLVDQOENGRVLVHALLACAEAVQENLTVAEALVKQIGFL 197
Db 211 AAPPATCGAAAAANAPVPPVVVDTQEAGIRLVHALLACAEAVQENFAAAEALVKQIPTL 270
QY 198 AVSQIGAMRKVATYFAEALARRIYRLSPSQSP-IDHSLSDLOMHFYETCPYLKFAHFTA 256
Db 271 AASOGGAMRKVAAVFEALARRVFRPADSTLLDAFADLLHAHFYESCPIYKFAHFTA 330
QY 257 NOALIEAFQGGKRRHVHIDFSMSQGLWPALMQALALRPGPPVFRLTGIGPPAPDNFDY 316
Db 331 NOALIEAFAGCHRVHVDVDFGKQGMWPAALQALALRPGPPSERLTGVPQPDDETAL 390
QY 317 HEVGCKLAHLAEAIHVEFYRGFVANTLADLASMELR-----PSEIESVAVNSVFLH 371
Db 391 QOVGWKLAQFAHTRVDFQYRGLVAATLADLEPFMLQPEGADANEPEVIANSVFLH 450
QY 372 KILGPPGAIDKVLGVVNOIKPEIETVVOESNHNHSPFLDRFTESLHYSTLFDLSLEGV 431
Db 451 RLLAQPGALEKVLGTVHVRPRIVTVVOEAEHNSGTFLDRTESLHYSTLFDLSLEGGS 510
QY 432 SGQ-----DKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGF 477
Db 511 SQOAELESPPAAGGGGTQDQVMSEVYLGKQICNVVACGAEATERHETLQWRNRLGRAGF 570
QY 478 AAHIGSNAPKQASMLLALFNGGEGYRVESDGCMLGWHTRPLIATSAMKLS 530
Db 571 EPVHLGSNAYKQASTLALFAGGEGYRVEEKDGCCLTLGWHTRPLIATSARVA 623

RESULT 9
Q9ST59 PRELIMINARY; PRT; 623 AA.
ID Q9ST59;
AC Q9ST59;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE GIBBERELLIN RESPONSE MODULATOR.
GN RHT-DIA.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99347734; PubMed=10421366;
RA Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
RA Flinham J.E., Beales J., Fish L.J., Worland A.J., Pellica F.,
RA Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
RT "Green revolution" genes encode mutant gibberellin response
RT modulators."
RL Nature 400:256-261(1999).
DR EMBL; AJ242531; CAB51555.1; -.
SQ SEQUENCE 623 AA; 65337 MW; F2BAC34996D0A84F CRC64;
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Query Match 57.8%; Score 1594; DB 10; Length 623;
Best Local Similarity 54.38; Pred. No. 3.6e-114;
Matches 332; Conservative 71; Mismatches 106; Indels 102; Gaps 11;
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QY 11 DKTTMMNEEDDGMDELLAVLGYKVRSEMDVAVKLEQLEVM-----SNVQEDD- 63
Db 22 EDKMWVSAAGAGEVDELLAALGYKVRASMDVAVKLEQLEMDMGVGGVAGAAPDGS 81
QY 64 -LSQATETVHYNPAELYTWLDSMLTDLNPP----- 93
Db 82 FATHLATDTVHYNPTDLSSWVESLSELNAPPPPLPAPQLNASTSTVTGGGCFDLP 141
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QY 94 -----SSNAEYDLKAIP-----GDAIL-----NOFAIDSASSNOGGGGDT 129
Db 142 SVDSSSIYALRPIPSAGATAPADLSADSVDPKRMRTGGSTSSSSSSSSSLGGG--- 198
QY 130 YTNRLKCSNGVVE-----TTTATAESTRHVVLDVDSQNGVRLVHALLACAEAVOKENL 184
Db 199 -----ARSSVWEAAPVVAANAATPALPVVVVDTOQAGRLVHALLACAEAVQOENL 250
QY 185 TVAEALVKOIGFLAVSOIGAMKRVATYFAELARRIYRL--SPSQSDIHSLSDTLQMHF 242
Db 251 SAAEALVKOIPILLASQGGAMKRVAYFGEALARRVFRFPQDSSLDDAAFDLLHAF 310
QY 243 YETCPYLKFAHTANOAILAEAFQKKRVHVIDFSMSQGLQWALMALRPGGPVFR 302
Db 311 YESCPLYLKFAHTANOAILAEAFAGRCRRVHVDFGKQGWQFALLQALALRPGGPSPFL 370
QY 303 TCGIGPAPDNFDYHEVGCKLAHLAEAHVEFEYRGVANTLADLASML-----ELRPS 357
Db 371 TGVGGPPQDETALQOVGWKLAQFAHTIRKDFQYRGLVAATLADLEPMLQPEGEEDPNE 430
QY 358 ETESVAVNSVFLHKLGRPGDAIDRVLGVNQIKPEIFTVVQECSNHNPIFLDRFTESL 417
Db 431 EPEVIAVNSVFEHMLLAQPGALEKVLGTVRAVRPIYTVVQECSNHNPIFLDRFTESL 490
QY 418 HYYSTFLDSLEG-----VPSGQDKVMSEVYLGKICNVVACDGPDRV 459
Db 491 HYYSTMFDSLEGSSGGGPPSEVSSGAAAAPAAAGTDQVMSEVYLGKICNVVACEGAERT 550
QY 460 ERHETLSQWRNFGSAGFAAHIGSNAPKQASMLLALFNGGEGYRVESEDGCLMLGWHTR 519
Db 551 ERHETLGQWRNLGNAGFTVHLGSNAYKQASTLLALFAGGQYKVEKEGCLTLGWHTR 610
QY 520 PLIATSAWKL 530
Db 611 PLIATSAWRLA 621
RESULT 10
Q9CBY3 PRELIMINARY; PRT: 511 AA.
AC Q9CBY3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GIBBERELLIN REGULATORY PROTEIN, PUTATIVE.
GN T27F4.10.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., L.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.";
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RL Nature 408:816-820(2000).
DR EMBL; AC020665; AAG52171.1; -.
SQ SEQUENCE 511 AA; 56754 MW; 1E60071697C92A9F CRC64;

Query Match 57.5%; Score 1587; DB 10; Length 511;
Best Local Similarity 59.0%; Pred. No. 9,1e-114;
Matches 319; Conservative 74; Mismatches 104; Indels 44; Gaps 9;

QY 1 MKRDHHHHQD-----KKTMMNEEDDNGMDLAVLGKYKVRSSPMADVAOKLEQLEVM 55
Db 1 MKREINHRESSAGEGSSMTVIKEEAAGVDLVLVIGKYKVRSSMDVAHKLQLEVM 60
QY 56 MSNVQEDDLSQLATETVHYNPAELTYTLWDSMLTDLNP-----PSSNAEYDLKAIPGDAINL 111
Db 61 LG----DGISLSDSETVHYNPSDLSCGWVESMLSDLPTRIQEKPDSEYDLRAIPGSAVVP 116
QY 112 QFAIDSASSSSNOGGGDTYTT--NKRKCSNGVVTATATAESTRHVVLDVDSQNGVRLV 169
Db 117 R-----DEHVTRRSKRTIESEL-----SSTRSVVVLDSQETGVRLV 153
QY 170 HALLACAEAVOKENLTVAEALVKOIGFLAVSOIGAMRVATYFAELARRIYRLSPSQSP 229
Db 154 HALLACAEAVQNNKLADALVKHVLGLASSOAGAMRVATYFAELARRIYRIPRDV 213
QY 230 IDHLSLSDTLQMHFYETCPYLKFAHTANOAILAEAFQKKRVHVIDFSMSQGLQWALMALQ 289
Db 214 ALSFSFDLTQIHFEYSCPYLKFAHTANOAILAEVFAEKVHVIDLGNHGLQWALMALQ 273
QY 290 LALRPGGPPVFRLTGIGPPAPDNFDYHEVGCKLAHLAEAHVEFEYRGVANTLADLDA 349
Db 274 LALRPGGPPDFRLTGIGYSLTD----IQEVGWKLQGLASTIGVNEFEKSIALLNNLSDLKP 329
QY 350 SMLELRPSEIESVAVNSVFLHKLGRPGDAIDRVLGVNQIKPEIFTVVQECSNHNPIFL 409
Db 330 EMDLIRPG--LESVAVNSVFLHKLGRPGDAIDRVLGVNQIKPEIFTVVQECSNHNPIFL 388
QY 410 LDRFTESLHYSTLFLDSLEGVPSGQDKVMSEVYLGKICNVVACDGPDRVERHETLSQWR 469
Db 389 LDRFTESLHYSTLFLDSLEGVPS--QDRVMSSELFGRQILNLVACGEDRVERHETLNQWR 447
QY 470 NEFGSAGFAAAHIGSNAPKQASMLLALFNGGEGYRVEESDGCMLGMLGWHTRPLIATSAWKL 529
Db 448 NREGLGGRKPVSGISNAYKQASMLLALYAGADGVNVEENEGCLLGLGWQTRPLIATSAWKL 507
QY 530 S 530
Db 508 N 508

RESULT 11
O65367 PRELIMINARY; PRT: 662 AA.
AC O65367;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAL PROTEIN.
GN RGA-LIKE.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COL-0;
RA Sanchez-Fernandez R., Ardiles-Diaz W., van Montagu M., Inze D.,
RA May M.J.;
RT "Cloning of the Arabidopsis thaliana RGA-like gene, a putative member
of the VHID domain transcription factor family.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ224957; CAA12242.1; -.
```

RA Sato S., Nakamura T., Kaneoka I., Sato C., Asamizu K., Nishikawa N.,  
RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RN  
RP  
RQ  
R1 EU Arabidopsis sequencing project;  
R2 Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
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QY 220 -----IYRLSP--SOSPIDHLSDTLQMHFYETCPYLKFAHFTANQAILEAFQGGKRVHV 272
Db 501 SSCLGIYATLPVSSHPTHNQKVASAFQV-FNGISPFVKFSHTANCAIQEAFEREERVHI 559
QY 273 IDFSMSOGLQWALPQALRPGGPPVFLTGIGPPADPNFDYLHEVGCKLAHLAEAIHV 332
Db 560 IDLDIMQGLQWPLGPHILASRPGGPPYVRLTGLG---TSMETLEATGKRLSDFANKLGL 615
QY 333 EFYRGF-VANTLADLDASMLELRPSEIESVAVNSVFLHKLGRPGAIDKVLGVVNOIK 391
Db 616 PEEF--FPAEKVGNIDVEKLVN--SKSEAVAVH--WLQHSLYDVTGSDTNTLWLLQRLA 669
QY 392 PEFTVVEQESNHNSPIFLDRTESLHYSTLFDLSL---EGVPSGQDKVMSEVYLGKQIC 448
Db 670 PKVVTWVEODLS-NAGSFLGREVEAIHYYSALFDSLGSYGSESEERHVVEQQLSREIR 728
QY 449 NVVACDGPDR---VERHETLSQWRNRFGSAGFAAAHIGSNAFKAQASMLLALFNGGEGYRV 505
Db 729 NVLAVGGFSRSEIRFH----NWREKLOCCGFRGVSLAGNATQASLLIGMF-PSEGYTL 783
QY 506 EESDGLMLGWHTRPLIATSAMK 528
Db 784 VEDNGILKLGWKDLCLLTASAWR 806

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